

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 23:36:27 ; Search time 5307.2 Seconds
(without alignments)
2006.538 Million cell updates/sec

Title: US-09-719-748-1_COPY_98_886

Perfect score: 789
Sequence: 1 tatgcacacgagagagct.....ctctacagacacccctgac 789

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estda: *
2: em_esthm: *
3: em_estln: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hlc: *
9: gb_estl: *
10: gb_estc2: *
11: gb_hlc: *
12: gb_gss: *
13: em_gss_hum: *
14: em_gss_liv: *
15: em_gss_pln: *
16: em_gss_vrl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------------|--------------------|
| 1 | 562.8 | 71.3 | 1729 | 11 AK004350 | AK004350 Mus muscu |
| 2 | 541.4 | 68.6 | 882 | 9 A1322362 | A1322362 me98c10.y |
| 3 | 501.4 | 63.5 | 830 | 10 BG688701 | BG688701 602787522 |
| 4 | 494.6 | 62.7 | 976 | 11 BC012210 | BC012210 Mus muscu |
| 5 | 483 | 61.2 | 972 | 10 B1554559 | B1554559 603235693 |
| 6 | 464.2 | 58.8 | 1199 | 11 AK009701 | AK009701 Mus muscu |
| 7 | 459.2 | 58.2 | 869 | 10 W82116 | W82116 me98c10.r1 |
| 8 | 428.2 | 54.3 | 671 | 10 BF727181 | BF727181 By17h06.y |
| 9 | 425.6 | 53.9 | 982 | 10 BF976537 | BF976537 602244391 |
| 10 | 422.2 | 53.5 | 585 | 10 BG384579 | BG384579 303638 MA |
| 11 | 414 | 52.5 | 708 | 9 AM476323 | AM476323 uc73f11.y |
| 12 | 413 | 52.1 | 649 | 10 B1046467 | B1046467 M33-EN020 |
| 13 | 411.4 | 52.3 | 1127 | 10 BE733365 | BE733365 601567911 |
| 14 | 410.6 | 52.0 | 555 | 10 BF087508 | BF087508 QV2-HT054 |
| 15 | 409 | 51.8 | 1058 | 10 BG421064 | BG421064 602451186 |
| 16 | 408.2 | 51.7 | 663 | 10 BF019568 | BF019568 ux12f12.y |
| 17 | 403.4 | 51.1 | 565 | 10 BF075625 | BF075625 224820 MA |

| | | | | | |
|----|-------|------|------|-------------|---------------------|
| 18 | 400.4 | 50.7 | 999 | 10 BF168866 | BF168866 601775325 |
| 19 | 394.4 | 50.0 | 556 | 10 BF075639 | BF075639 224840 MA |
| 20 | 394.4 | 50.0 | 696 | 10 BF021203 | BF021203 ux53901.y |
| 21 | 391.4 | 49.6 | 871 | 10 B1690902 | B1690902 603312045 |
| 22 | 386 | 48.9 | 681 | 10 B1194425 | B1194425 602848986 |
| 23 | 385.4 | 48.8 | 797 | 10 B1663166 | B1663166 603286787 |
| 24 | 385.2 | 48.8 | 887 | 10 BG968191 | BG968191 602835674 |
| 25 | 379 | 48.0 | 855 | 10 B1828782 | B1828782 603074924 |
| 26 | 378 | 47.9 | 703 | 10 BG65492 | BG65492 602783624 |
| 27 | 377 | 47.8 | 1039 | 10 BG419640 | BG419640 602451855 |
| 28 | 376.2 | 47.7 | 756 | 10 BF162798 | BF162798 601769262 |
| 29 | 372.4 | 47.2 | 460 | 9 AA858002 | AA858002 of63908.s |
| 30 | 371.4 | 47.1 | 654 | 10 B1012312 | B1012312 B0132018 |
| 31 | 370.4 | 46.9 | 796 | 10 BG421646 | BG421646 602449739 |
| 32 | 365.2 | 46.3 | 481 | 9 AM603538 | AM603538 RC0-CN002 |
| 33 | 363.8 | 46.1 | 710 | 10 BG277312 | BG277312 ux42b06.y |
| 34 | 358.8 | 45.5 | 785 | 10 B1652999 | B1652999 603299971 |
| 35 | 355.8 | 45.1 | 707 | 10 B1904738 | B1904738 603168651 |
| 36 | 352.2 | 44.6 | 798 | 10 BG682263 | BG682263 602795880 |
| 37 | 345.8 | 43.8 | 636 | 9 AA557328 | AA557328 n181a06.s |
| 38 | 345.8 | 43.8 | 693 | 9 AL631486 | AL631486 AL631486 |
| 39 | 343.6 | 43.5 | 616 | 10 B1791576 | B1791576 1G99006.x |
| 40 | 342.8 | 43.4 | 622 | 10 B1414743 | B1414743 602991133 |
| 41 | 341.6 | 43.3 | 589 | 9 AM421982 | AM421982 f189d06.y |
| 42 | 339 | 43.0 | 958 | 10 B1757256 | B1757256 603030761 |
| 43 | 338.8 | 42.9 | 743 | 10 BG968192 | BG968192 602835675 |
| 44 | 337.8 | 42.8 | 623 | 10 BE848999 | BE848999 ux01907.y |
| 45 | 326.8 | 41.4 | 1300 | 10 BF685010 | BF685010 6021242870 |

ALIGNMENTS

| | | | | | |
|------------|--|-------------|------|--------|-----------------|
| RESULT 1 | AK004350 | 1729 bp | mRNA | linear | HTC 19-JAN-2002 |
| LOCUS | AK004350 | | | | |
| DEFINITION | Mus musculus 18 days embryo whole body cDNA, RIKEN full-length enriched library, clone:1110062102:death-associated kinase 2, full insert sequence. | | | | |
| ACCESSION | AK004350 | | | | |
| VERSION | AK004350.1 | GI:12835501 | | | |
| KEYWORDS | HTC; CAP trapper. | | | | |
| SOURCE | Mus musculus (strain:C57BL/6J) 18 days embryo cDNA to mRNA, clone:1110062102. | | | | |
| ORGANISM | Mus musculus | | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. | | | | |
| AUTHORS | Carninci,P. and Hayashizaki,Y. | | | | |
| TITLE | High-efficiency full-length cDNA cloning | | | | |
| JOURNAL | Meth. Enzymol. 303, 19-44 (1999) | | | | |
| MEDLINE | 99279253 | | | | |
| PUBMED | 10349636 | | | | |
| REFERENCE | 2 (sites) | | | | |
| AUTHORS | Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y. | | | | |
| TITLE | Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes | | | | |
| JOURNAL | Genome Res. 10 (10), 1617-1630 (2000) | | | | |
| MEDLINE | 20499374 | | | | |
| PUBMED | 11042159 | | | | |
| REFERENCE | 3 (sites) | | | | |
| AUTHORS | Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuami,T., Tashiro,H., Itoh,A., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsunoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujikake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunaga,S., Kawai,D., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A., and Hayashizaki,Y. | | | | |
| TITLE | RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer | | | | |
| JOURNAL | Genome Res. 10 (11), 1757-1771 (2000) | | | | |


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Oy 181 caccacaatgcatcagctcgcacagcgtctatgaaacccgacgctggtgacatc 240
Db 359 CACCCCAACATCATCACCTGACAGAGCTATGAGAACCCAGCAGCTGCTCTATC 418
Oy 241 ctgagcagctgctcgcagcagcctctgacatctctctgcccagaagagctactgagt 300
Db 419 CTTGAGCTAGTGTCCGAGGAGAACTGTTGATTTCTGCCCCGAAAGAGTGTAGT 478
Oy 301 gaggagagagccacacagctcattaaagacagatccctgagtgaggtgacactccacac 360
Db 479 GAGAGAGAAAGCCACACCTCATTAAGCAGATCCTGATGGGTGAATTAACCTTCACACA 538
Oy 361 aagaaatctcctcacttgatctcctcagccagaataacattatgtgtta-gacagaatat 419
Db 539 AAGAAATGCTCAGCTTGTGATCTCAAGCCAGAAACATCATGTTGTTACAGACAAGATAT 598
Oy 420 tccactccacacatcaagctgattgactgtgtctgcccacagaataagagatgga-g 478
Db 599 CCCCATCCACACATCAAGCTGATGTACTTGGCTGGCTCAGGAAATGAAAGATGAGAG 658
Oy 479 ttgaattagaataatt-ttggagacgcggaattgtgtgtctccagaataattgaaactac 537
Db 659 TTGAATTTAAACATGTTTGGGACACCTGATTTGTTGCTCCAGAAATCGTGAACATAT 718
Oy 538 gaggccctggg-ctgagagcctgacatgtgagcagatagcgtcattacactacatccctt 596
Db 719 GAGCCATGGGAGACTGAGATGGCACTGTGAGCATTTGAGTCACTCACTTAATACCTTCT 778
Oy 597 aagtgagacatccctcttccctgggagacagagacaggaacacgtggcaaat 648
Db 779 AAGTGGAGGCTGCCCTTCTCTGGAGAGACAAAGAAACCCCTGGCAATAT 829

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RESULT 4
LOCUS BC012210 976 bp mRNA linear HTC 08-AUG-2001
DEFINITION Mus musculus, Similar to Death-associated like kinase, clone
IMAGE:3993055, mRNA.
ACCESSION BC012210
VERSION BC012210.1 GI:15126556
KEYWORDS HTC.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Strausberg, R.
Direct Submission
Submitted (06-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.ncl.nih.gov
Contact: MGC help desk
Email: gcgaps-remail.nih.gov
Tissue Procurement: Lohar Hemmighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalobebcm.tmc.edu.
Villalob, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Hollway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.

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REMARK COMMENT

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov> Series: IRAP Plate: 23 Row: n Column: 16 This clone was selected for full length sequencing because it passed the following selection criteria: Genomescan gene

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FEATURES
source
prediction, similarity but not identity to protein
This clone has the following problem: incomplete processing.
Location/Qualifiers
1..976
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_image="3993055"
/tissue_type="Mammary tumor. MAP-TGF alpha model. 7 months
old, gross tissue."
/clone_id="NCL CGAP_Mam5"
/lab_host="DHI0B"
/note="Vector: pCMV-SPORT6"
BASE COUNT 240 a 271 c 294 g 171 t
ORIGIN
Query Match 62.7% Score 494.6 DB 11 Length 976;
Best Local Similarity 76.7% Pred No. 6.4e-109;
Matches 605; Conservative 0; Mismatches 184; Indels 0; Gaps 0;
Oy 1 tatgacatcgagagagagctgaggagtgccagttgcccactgtgaagaagtgccggag 60
Db 131 TATGAGATGGAGAGAGAGACTTGGCAGATGTCGCAATTTGGCATCGTCCGCAATGCCACAG 190
Oy 61 aagaacaggggcttgagtgatgagccaagtctcaagaagcggcagagcgagc 120
Db 191 AAGGCGAGGCGCATGAGATATGACGCCAAGTTCTATCAAGAAAGCGGCCCTGCTCCATCCAGC 250
Oy 121 cggcgcggtgtgagcgggagagatcgagcggaggtgagcatccctcgcgcgagtgctg 180
Db 251 CGGCGCGGTGTGAGCCCGGAGAGATCGAAGCGAGGTGAGCATCCGCGCGAGATCCG 310
Oy 181 caccacaatgcatcagctcgcacagcgtctatgagaaacccagcagctggtgacatc 240
Db 311 CACCCCAACATCATTAACATGCTGATGAGTGTGAGAAACAGACAGATGTGTGTGATGAT 370
Oy 241 ctgagcagtgctcgtgagagagctctcgtatctcctgcccagaagagagtgacagagt 300
Db 371 CTGAGCTGTGTGTCGGGTGGAGACTTTTGACATCTCTGCGCCAGAAAGAGATATTGAGC 430
Oy 301 gaggagagagccacagctcattaaagcagatctcgtatgagggtgaaactacactcacaca 360
Db 431 GAGGATGAGGCCACGCGCATGTTCTCAAAACAAATCTTGAGCGTGTCCATACCTGCACCTCC 490
Oy 361 aagaaatgtctcactctgacatcgaagcagaagaataatattgtgtgacaagaatat 420
Db 491 AAGCGCATCGCACATTTGACCTGAGAGCCCGAGAACATCATGTTGCTGAGCAAGCAGCA 550
Oy 421 cccattccacacatcaagctgattgacttggctcgtcaccagaataaagaatgagtt 480
Db 551 GCCAGCCCGCGCATTAAGCTCATGCACTTGGCATCGCGCACAGATGAGGCTGGCAGC 610
Oy 481 gaattaaagaatatttttggagccgcggaattgtgtgtccagaataattgtgaactagag 540
Db 611 GAGTTCAAAACATCTTTTGGACACCCGAGTTGTGCCCCCGAGATGATGTAATATGAG 670
Oy 541 cccctgggtctgagagcctgacatgtgagcagatagcgcatacctaactaactccttaagt 600
Db 671 CCACCTGGCTGAGAGCTGACATGTGAGAGCATTTGCGCTCATACCTTAATATCTCTGAGC 730
Oy 601 gggagatcccttctcctgaggagacagagaagaagaacactgagcaaatatcacatcagtg 660
Db 731 GGAGGCTCCCATCTTCTTGGGAGACCAAGCAGAGAGAGATGAGCAATCTCGACAGTG 790
Oy 661 agtgcagacttgatgagaaattctcagcattcgagcagcgagcgtggccagaagacttaatt 720
Db 791 AACTATGACTTTGATGAGAGATTAATTCAAGCAGCAACGCGAGCTGGCCAAAGACTTCATC 850
Oy 721 cggaaagctctgtttaaagagacccggaaagagcgtccacatccaagagcctctcaagcac 780
Db 851 CGAGGCTGCTGTCAAGAACCCCAAGAGAGAGATGACATCGACAGAGGCTGAGGACT 910
Oy 781 cccctgagtc 789

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Db 911 TCCGCGATC 919
|||||||
|||||||
|||||||

RESULT 5
BI554559 972 bp mRNA linear EST 05-SEP-2001
LOCUS 603235693F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:5310046 5',
DEFINITION mRNA sequence.
ACCESSION BI554559 GI:15441873
VERSION BI554559.1
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 972)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L19M1785 row: 1 column: 23
High quality sequence stop: 845.
Location/Qualifiers
1..972
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5310046"
/clone_1lb="NCI_CGAP_L19"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: Liver; Vector: pCMV-Sp6R6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 239 a 269 c 298 g 166 t

ORIGIN

Query Match 61.2%; Score 483; DB 10; Length 972;
Best Local Similarity 77.5%; Pred. No. 4e-106;
Matches 585; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

Db 1 tatgaacatcgagagagctgaggagctgagccagcttcgcatcgtagaagagtgccggag 60
|||||
Db 32 tatgagatgagagagagcttgcgacgtgagccatgtgcatctgagccagatgacagag 91
|||||
Db 61 aagagcaggggcttgtagatgacgcaagctcacaagaagcgagcgagcgagcgagc 120
|||||
Db 92 aaggcagcgagctgagatgacgcaagctcacaagaagcgagcgagcgagcgagc 151
|||||
Db 121 cggcgagctgtagcggagagagatcgagcgagagtgagcatcctcgcgagagtgctg 180
|||||
Db 152 cggcgagctgtagcggagagagatcgagcgagagtgagcatcctcgcgagagtgctg 211
|||||
Db 181 caccacaatgcatcagcgtcgacgagctctatgagaacgcgacgcagcgagtgtagc 240
|||||
Db 212 caccaccaatgcatcagcgtcgacgagctctatgagaacgcgacgcagcgagtgtagc 271
|||||
Db 241 cttagagtagtgctgtagagagagctctgattccctgagcccgagagagtagcagct 300
|||||
Db 272 ctgagagctggtgctcggcgagcctttgacattcctgagcgaagagagtagcagc 331
|||||
Db 301 gaggagagagcgacacagctcatcaagagagctcctgagtgaggtagaactacatcaca 360
|||||

Db 332 GAGGATGAGGGCCAGCAGCTTCCTCAACAATCTAGACGGTGTTCACCTACCTGCACTCC 391
Oy 361 aagaaatgctcaacttgatcctcaagccagaataatattgttttagaagaatatt 420
|||||
Db 392 AAGGCAATCGCAGCACTTGTGACCTGAGGCCGAGAACATCATGTGTGGACAACGCGCA 451
Oy 421 cccatccacacatcaagctgattgacttgctgtgctcgcgaataatgagagagatt 480
|||||
Db 452 GCCAGCCCCCGCATTAACCTCATGCACTTGTGGCATCGCGCAGAGATGAGGCTGGCAGC 511
Oy 481 gaattagaatatttttgagagcgccggaatttctgtctccagaatattgtaactagag 540
|||||
Db 512 GAGTTCAAGAACATCTTGTGGCACCAGGATTTGTGGCCCCGAGATGTTGAATATAG 571
Oy 541 cccctgggtctgagagctgacatgtgagcatalaggcgatcattacattccttaagt 600
|||||
Db 572 CCACCTGGCTTGTGAGAGCTGACATGTGGAGCATTTGGCGTCATCACTTCACTCTTGAGC 631
Oy 601 gggagatcccttcctctgagagacagagagaggaagaacacggaatatacatcagtg 660
|||||
Db 632 GGAGGCTCCCATTTCTGTGGGAGACCAAGAGAGAGCTGACGACATCTTCACTGAG 691
Oy 661 agtiacgacttgatgaggaattctcagccatacagagagagctggtcccaagacttatt 720
|||||
Db 692 AACATGACTTGTGATGAGGATTAATCTTCAAGCAGCAGCAGCTGGCCAGAGCTTCAATC 751
Oy 721 cggagagcttctggttaagagagacccggaagagct 755
|||||
Db 752 CGCAGGCTGTGTCAAGAGCCCAAGAGAGAGAT 786
|||||

RESULT 6
AK009701 1199 bp mRNA linear HTC 19-JAN-2002
LOCUS Mus musculus adult male tongue cDNA, RIKEN full-length enriched
DEFINITION library, clone:2310039H24:DEATH ASSOCIATED PROTEIN KINASE, full
insert sequence.
ACCESSION AK009701 GI:12844657
VERSION AK009701.1
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA,
clone:12310039H24.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2 (sites)
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 11042159
PUBMED 20499374
REFERENCE 3 (sites)
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, O., Nishi, K., Kitsumaki, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, S., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multipillar sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 11076861
PUBMED

| | | | |
|------------|--|---|-----------------------------|
| Db | 300 | TCAAGCTGATTTGGCTTGTGGCTGCACGAATTGAAAGATGGACTTAATTTAAAAACA | 359 |
| Oy | 494 | tcttttgagacgcgggaatttgcgtccagaatactgtaactacgagccctcggtc | 553 |
| Db | 360 | TTTTTGGGACACGTAATTTGTGTGTCACGAATCGTAACATANGAGCCACTGGAC | 419 |
| Oy | 554 | aagcttcacatgttgtagcatagaggctcatcacctaccatccctcttaagtga | 613 |
| Db | 420 | AGGGCGACATGTGGAGCATTTGGAGTCATCACCTTATCTTCTTAAGTGAGAC | 479 |
| Oy | 614 | tcccggagagacgaagaagaacaacctcggcaaatatcacatcagttgagta | 673 |
| Db | 480 | TCCTGGGAGACACGAAACAGAAMAC-CTGGCAATAAT- ACTGCTTTAAGTTAC | 537 |
| Oy | 674 | atggaagatcttcagcatatcagagcgagcgtcgccaagacttatctcgaag | 733 |
| Db | 538 | ATTAGAAATGCTCAGGCC-GGCCAAGAGAGCTGGCCAAG-CTTATTCGGAAG | 595 |
| Oy | 734 | ttaa ttaa ttaa ttaa ttaa ttaa ttaa ttaa ttaa ttaa ttaa | 797 |
| Db | 596 | TGAA TGAA TGAA TGAA TGAA TGAA TGAA TGAA TGAA TGAA | 650 |
| RESULT | 8 | | |
| LOCUS | BF727181 | 671 bp | mRNA linear EST 05-JAN-2001 |
| DEFINITION | bf17n06.y1 Human Lens cDNA (un-normalized, unamplified): BY Homo sapiens cDNA clone bf17n06 5', mRNA sequence. | | |
| ACCESSION | BF727181 | | |
| VERSION | BF727181.1 | GI:12043092 | |
| KEYWORDS | EST. | | |
| SOURCE | human. | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. | | |
| AUTHORS | Wistow,G.J., Bernstein,S., Behal,A. and Smith,D. | | |
| TITLE | NEIBANK: EST analysis and bioinformatics for ocular genomics | | |
| JOURNAL | Invest. Ophthalmol. Vis. Sci. 41 (2000) In press | | |
| COMMENT | Contact: Wistow G Section on Molecular Structure and Function National Eye Institute 6/331, NIH, Bethesda, MD 20892-2740, USA Tel: 301 402 3452 Fax: 301 496 0078 Email: graeme@helix.nih.gov Plate: 17 row: h column: 06 Seq primer: M13Rpl reverse primer (ABI). Location/Qualifiers 1..671 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="bf17n06" /cGene_id="Human Lens cDNA (Un-normalized, unamplified): By" /issue_type="Lens" /dev_stage="Adult" /lab_host="EMDH10B" /note="Organ: Eye; Vector: pcMVSPORT6; Two human lenses from different adults (both approximately 40 years old) together yielded 20ug of total RNA and 150ng mRNA for CDNA library synthesis. A directionally cloned cDNA library in the pcMVSPORT6 vector was constructed at Life Technologies , essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetechn.com/). First strand synthesis was carried out using a Not I primer-adaptor [5'-cgacatgctctagatcgccgagcgccgcc(7)15-3']. Not I/blunt end inserts were cloned into the Not I/EcoR V sites in the vector. EST analysis was performed on the unamplified library at the NIDDK Intramural Sequencing Center (NISC)." | | |

| | | | |
|---|---|--|-----------------------------|
| Db | 541 | GAGACCAAGCAGGAGAGCGCTCACCAACTTCACGGCGTGAACCTAGACATTGTGACAGAGAG | 600 |
| OY | 682 | tcttcagcatalacgagcgagctggccaaaggacttalcggaaagctctgtttaagag | 741 |
| Db | 601 | TACTTACACAACACCAGCAGGAGCTGGCCAAAGCATTTATTCGCCGCTCTCGTCAAGA | 660 |
| OY | 742 | nccc 745 | |
| Db | 661 | TCCC 664 | |
| <hr/> | | | |
| RESULT 10 | | | |
| LOCUS | BC384579 | 585 bp | mRNA linear EST 12-MAR-2001 |
| DEFINITION | 303638 MARC 1Pig Sus scrofa cDNA 5', mRNA sequence. | | |
| ACCESSION | BC384579 | | |
| VERSION | BC384579.1 | GI:13308988 | |
| KEYWORDS | EST. | | |
| SOURCE | pig. | | |
| ORGANISM | Sus scrofa | | |
| REFERENCE | Eukariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus. 1 (bases 1 to 585) Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keeler,J.W. Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000) | | |
| JOURNAL | Contact: Smilh TPL | | |
| COMMENT | USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel.: 402 762 4366 Fax: 402 762 4390 Email: smilhemail.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options. PCR primers FORWARD: AGGAACAGCTATGACCAT BACKWARD: GTTTCAGTGACGACGAG Plate: 91 row: M column: 15 Seq primer: ATTAGGTGACACTATGAG. Location/Qualifiers 1..585 /organism="Sus scrofa" /db_xref="taxon:9823" /clone_lbp="MARC 1Pig" /_tisue_type="pooled" /_lib_host="DH10B" /_note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos." | | |
| <hr/> | | | |
| BASE COUNT 137 a 159 c 178 g 111 t | | | |
| ORIGIN | | | |
| <hr/> | | | |
| Query Match 53.5%; Score 422.2; DB 10; Length 585; | | | |
| Best Local Similarity 94.0%; Pred. No. 1.6e-91; | | | |
| Matches 439; Conservative 0; Mismatches 28; Indels 0; Gaps 0; | | | |
| OY | 1 | tatgcatactgagaaggaagctgggggttgccagtcttcacatcgttaagaagtcgagag | 60 |
| Db | 119 | TACGACATCTGGGAGAGAGACTGGGAGCGGCAGTTTGCATCTGTAAATAAGTCCGGAG | 178 |
| OY | 61 | aagagcacggggccttagtatgcagcaaatcatcaaagcggcagagaccggcgagc | 120 |
| Db | 179 | AAGACACAGGGGACTGGAATACGCCCCCAAATTCAACAAGCGCAGCGCGGCGAGC | 238 |
| OY | 121 | cggcgcggttgagagcgcggtgagagatcgagcgggaggtgagacatctctgcgagtgctg | 180 |
| Db | 239 | CGGCGGGCGCTGTCGGGGAAGAAGATTGAGCGGGAGGTGGCATCTTCGCGCAGGCTGTG | 298 |

| | | | | |
|---------------------|---|--|--|------------------------|
| Oy | | 181 | caccacaatgtcctacagcttcgaagaactcatgaaagcacccgcggcggtgacctac | 240 |
| Db | 299 | CACCCCAAGTCATCACGCTCAGACGCCTTTGAAGAACCACCGACGGTGTCTCATC | 358 | |
| Oy | 241 | cttagagtacgtctcgaggagagactcttcgatccccttgscgccagaagagtaactgagt | 300 | |
| Db | 359 | CTCAGAGTAGTGTCGTGGAGAGAGACTGTTGCACATTCCGTGGGCCAAGAAGAACTCCCTGAGT | 418 | |
| Oy | 301 | gaggagagsgccaaccaagcttcaataagacagalccctgtagtgggtgtaactlaccacaa | 360 | |
| Db | 419 | GAGGAGGAGCGGACACAGCTTCATTAAACAGATCCTGGAGTGGGGTAACAATACTTCATCC | 478 | |
| Oy | 361 | aagaaaattgctaactttgatctcaaagccaaaaaacattaagtgttagaagaagaatat | 420 | |
| Db | 479 | AAGAAAATTGCTCACTTTGATCTCAAAGCCAACAAAAACATTAAGTTGTTGGACAAGAATAT | 538 | |
| Oy | 421 | ccccatccacacatcaagaacttatgacttgaacttgtctgycgcacgaaat | 467 | |
| Db | 539 | CCCCATCCACATCAAGCTGATTGACTTTGGCTGGCCTGCCTCATGAAT | 585 | |
| RESULT | 11 | | | |
| LOCUS | AW476323 | 708 bp | mRNA | linear EST 24-FEB-2000 |
| DEFINITION | AW476323 | ug73fll.y1 NCI-CGAP LuJ3 Mus musculus cDNA clone IMAGE:2936781 5' | | |
| VERSION | AW476323 | similar to TR:O54784 O54784 DEATH-ASSOCIATED KINASE 3 ; , mRNA sequence. | | |
| KEYWORDS | AW476323.1 | GI:7046429 | | |
| SOURCE | Eukarya; | | | |
| ORGANISM | Mus musculus | | | |
| REFERENCE | 1 (bases 1 to 708) | | | |
| ADDITIONAL COMMENTS | NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.National Cancer Institute; Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Other ESTs: ug73fll.x1 Contact: Robert Strausberg, Ph.D. Email: cgapds-femail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: www-bio.lnl.gov/bdrp/image/image.html | | | |
| JOURNAL COMMENT | MGI:1049201 | | | |
| FEATURES | Seq primer: -40RP from Glbcoc High quality sequence stop: 471. Location/Oualifiers 1..708 /organism="Mus musculus" /strain="CZECH II" /db_xref="taxon:10090" /clone="IMAGE:2936781" /clone_id="NCI_CGAP_LuJ3" /tisue_type="Pooled lung tumors" /lab_host="DH10B (phage-resistant)" /note="Organ: Lung; Vector: pUT73D-Pac (Pharmacia) with a modified polylinker: Site_1: NotI; Site_2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAATGAGGAGCGCGCTGTTTTTTTTTTTTTTT 3'] . Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pUT73 vector. Library went through one round of normalization, and was | | | |

Db 221 CGAGTCGCCAGAGACTTTATTCGGAAGCTTCTGTTAAAGAGACCCGGAAAGGCTCAC 162

QY 759 aatcaagaggctctcaagacccttgatc 789

Db 161 AATCAAGAGGCTCTCAGACACCCCTGGATC 131

RESULT 13

BE733365 1127 bp mRNA linear EST 15-SEP-2000

LOCUS 601367911F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842667 5',

DEFINITION mRNA sequence.

ACCESSION BE733365

VERSION BE733365

KEYWORDS EST.

SOURCE BE733365.1 GI:10147357

ORGANISM human.

REFERENCE NIH-MGC http://mgc.ncl.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgabbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: Image.Lnl.gov

Plate: L1CM536 row: e column: 04

High quality sequence stop: 723.

FEATURES

source 1..1127

Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3842667"

/clone_1lb="NIH_MGC_21"

/tissue="choriocarcinoma"

/lab_host="Dh10b (phage-resistant)"

/note="Organ: Placenta; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 268 a 305 c 357 g 197 t

ORIGIN

Query Match 52.1%; Score 411.4; DB 10; Length 1127;

Best Local Similarity 74.1%; Pred. No. 8.1e-89;

Matches 354; Conservative 0; Mismatches 186; Indels 1; Gaps 1;

QY 1 tatgacatcgagagagagctgagagatgagcagcttgcacatgtaagaagtgccggag 60

Db 184 TATGAGATGGGGAGGAGCTGGGACGGCGGAGTTTCGATCGTGGGAAGTGGCGGAG 243

QY 61 aagaagcaggggcttgagctgacgcaaatcatcaagaagagcgagagccggggagc 120

Db 244 AAGGGCCGGGGCAAGGAGTACGCAAGCCAAAGTTCATCAAGAGCCCGCTGTATCCAGC 303

QY 121 cggcgagtgagcagcgagagatcgagcgagagtgagcatcctcgcgagtgctg 180

Db 304 CGGCGTGGGGTGGAGCCGGAGAGATGAGCGGAGGTGAACATCTCGCGGAGATCCG 363

QY 181 caccacaatgcatcagcgtgacgagcgttatatgagaacccgacccgagcgtgtagcac 240

Db 364 CACCCCAATCATACACCTCGACAGCATCTTCGAGAAACAGGAGCGTGGTCTCATC 423

QY 241 ctgagctagtgctgagagagagctcttcgattcttcctggcccaagaagagtcagt 300

Db 424 CTGAGCTGCTCTCTGTGGCGGGAGACTCTTTGACTCTCTGGGGAGAGAGTGGCTGACG 483

QY 301 gagagagagccaccagctcaatcaagacatcctgtagtgaggtagtaacctcacaca 360

Db 484 GAGAGCAGGACCAACCCAGTTCTTCACAGACATCCCTGGACGGCGTTCACTACCTGACTCT 543

QY 361 aagaagaatgctcaacttgatctcaagccaagaacatctgtgttagcaagaataatc 420

Db 544 AAGCGATCGCACCTTTGACCTGAAGCCGAAAAACATCATGCTGTGGACAAAGACGTG 603

QY 421 cccatccacaacatcaagcagatgacttgctgctgcgtcagcaagaatagaagatgag 480

Db 604 CCGACCCAGCATCAAGATCATGACTTCGGCATTCGCCGACAGATCGAGCGGGAGAC 663

QY 481 gaattagaataatttggagcgcggaatttgctccagaatltgtaactagag 540

Db 664 GAGTTCAAGAACATCTTCGGACCCCGAGTTTGTGGCCCGAGAGATTGTAACATAGAG 723

QY 541 cccctggtctgagagctgagcatgtagagcatagcgctcaactacatccttcaagt 600

Db 724 CCGCTGGGCTTGGAGGGGAGCATGTGAGCATCGTGTCAATCACTTATCTCTGAGGG 783

QY 601 ggaagcatccctctcctgagagacagcagaagaacactgggaatatcacatcagt 660

Db 784 TGAATTCCTCGGTACCTTGGCGAAGACCAAGGACAGACGCTCACAGATTCGAGCCT 842

QY 661 agttacgacttggtaggaattctcagccatcagcagcagctggcgaaggaattatc 720

Db 843 AACACAGACTTCGACAGAGAGTCTTAGAAACCAAGCTAAGTTGGCGAGAGGTTGATC 902

QY 721 c 721

Db 903 c 903

RESULT 14

BF087508/c 555 bp mRNA linear EST 19-OCT-2000

LOCUS QV2-HT0541-130900-364-d03 HT0541 Homo sapiens cDNA, mRNA sequence.

DEFINITION BF087508

ACCESSION BF087508

VERSION BF087508.1 GI:10893218

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?fl=6tz-QV2-HT0541-130900-364-d03&tz=2000-09-13&tz=1>)

Seq primer: puc 18 forward

High quality sequence start: 4

High quality sequence stop: 555.

Location/Qualifiers

source

1. 555

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="HM0541"

/dev_stage="Adult"

/note="Organ: head,neck; Vector: puc18; Site_1: SmaI;

Site_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

BASE COUNT

127 a 140 c 134 g 154 t

ORIGIN

Query Match

Best Local Similarity 99.0%; Score 410.6; DB 10; Length 555;

Matches 413; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

373 cacttgcattcacaagcagaacacattatgtttagacaagaatatccattccacac 432

555 CACTTGATCTCAAGCCAGAAACATTATGTTTGTAGACAAGATATCCATTCCACAC 496

433 atcaagctgattgacttgctgtctgctcagaataagatgagttgaattaaagat 492

495 ATCAAGCTATGACTTGTGCTGCTCAGAAATAGAAAGATGAGTTGAATTAAGAA 436

493 atttttgagcgcgcgaattgttgcctcagaataatgtgaacagagccctgggtc 552

435 ATTTTGGGACGGCGGAATTTGTTGCTCCAGAAATTTGTACACAGACGCCCTGG 376

553 gaggctgacatgttgagcatagagcgctacacacacacacacacacacacacac 612

375 GAGGCTGACATGTGAGCATAGCGCTCATACCTACATCCTCTTAGTGAGAGATCC 316

613 ttccctggagagacagaagaagaagaacacacacacacacacacacacacacac 672

315 TTCCTGGGAGACACAGAAAGAGAAACACTGSCAAATATACAGCACTGATACGCT 256

673 gatgaggaattcttcagccatacagagcagcgtgcagcaagacttaattcgaga 732

255 GATGAGGAATTTCTTCAGCCAGACGAGCGAGCTGGCAAGACTTATTGGGAAGCT 196

733 gftaaagagaccggaaagcgtcacaatcaagaagcgtctcaagaacccctgagc 789

195 GTTAAAGAGACCCGGAAACGGCTCAATCCAAAGAGGCTCTCAGACACCCCTGAT 139

Db

RESULT 15

Bg421064

LOCUS

602451186f1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4589709 5',

DEFINITION

mRNA sequence.

ACCESSION

Bg421064

VERSION

Bg421064.1 GI:13327479

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1058)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaabs-remail.nih.gov

Tissue Procurement: DCM/D/DRP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: LLCML323 row: k column: 22

High quality sequence stop: 615.

Location/Qualifiers

1. 1058

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="IMAGE:4589709"

/clone_lib="NIH_MGC_14"

/issue_type="renal cell adenocarcinoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRV/XhoI sites using the following 5'

adapter: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT

295 a 278 c 339 g 146 t

ORIGIN

Query Match

Best Local Similarity 77.6%; Score 409; DB 10; Length 1058;

Matches 507; Conservative 0; Mismatches 145; Indels 1; Gaps 1;

40 atctgtaagaagtgtccgagagaagcagcgggtctgagatcagcccaatcacaag 99

2 ATCTGTGAGAGAGTCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 61

100 aagcggcagagccggcggcggcggcggcggcggcggcggcggcggcggcggcgg 159

62 AAGCGCGCGCTGTGATCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 121

160 agcatctcggcaggtgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 219

122 AACATCTCTCGGAGATCCGGGACCCCAACATCATACCTGACACATCTTTCGAAAC 181

220 cgcacccagcgtgtcgaacatccttgagcgtgagctgagcgtgagcgtgagcgt 279

182 AAGAGGAGAGTGTCT 241

280 gcccaagagagtcagctgagtgagtgagtgagtgagtgagtgagtgagtgagtg 339

242 GCGGAGAGAGTCTCCGTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 301

340 ggggtgaactacatcacaagaagaatgtcatttcatttcatttcatttcatttc 399

302 GCGCTTCACTACCTCCTCACTCACTCACTCACTCACTCACTCACTCACTCACT 361

400 atgtgttagagaagaataatccattccacacatcaagaagcgtgagctgtgagct 459

362 ATGCTGTGAG 421

460 cagcaaatagagaatgagatggaatttaagaatatcttgaggagcgggaatttttct 519

422 CACAGAGATCGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 481

520 ccagaatctggaactcagagcccttggtctgagagcgtgagcgtgagcgtgagcgt 579

482 CCAGAGATGTGACTATGAGCCGCTGGGCTGGAGGCGGAGCATGTGAGCATGCTG 541

580 atcaactacatcccttcaagtgagagcagccttcccttgaggagagacagaagaaga 639

542 ATCACTATATCTCTCTGAGGCGGTGATCCCGTTCTTCTGAGGAGAGAGAGAG 600

640 ctggcaaatcacatcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 692

601 CTCACCAAGATCTCAGCGGTGACTACAGAGTCCAGAGAGAGAGAGAGAGAGAG 653

Db

Sat May 18 15:09:07 2002

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Page 13

Search completed: May 17, 2002, 23:36:36
Job time: 5495 sec

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